

Figure 1

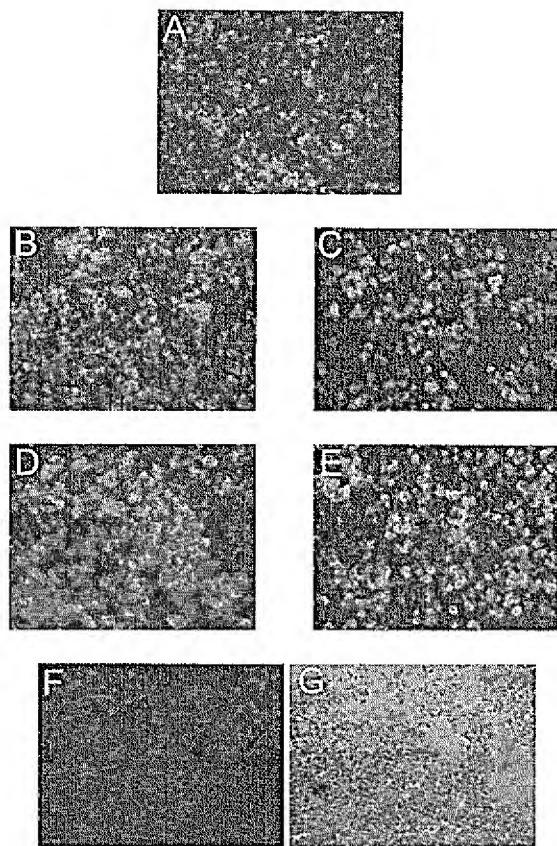


Figure 2

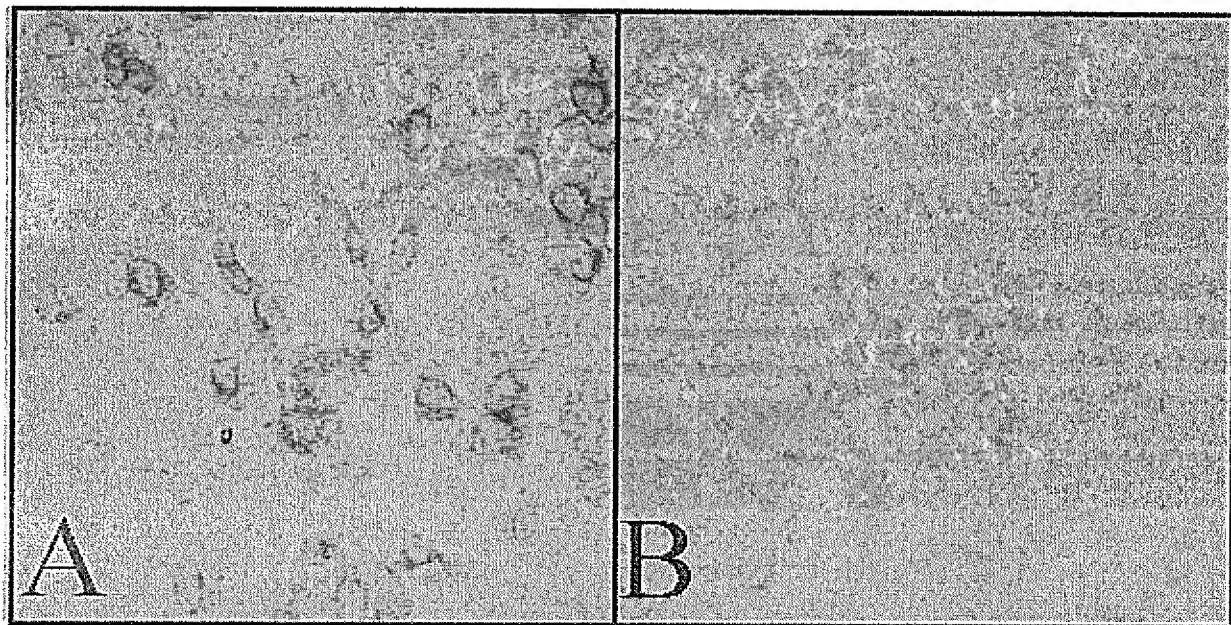


Figure 3

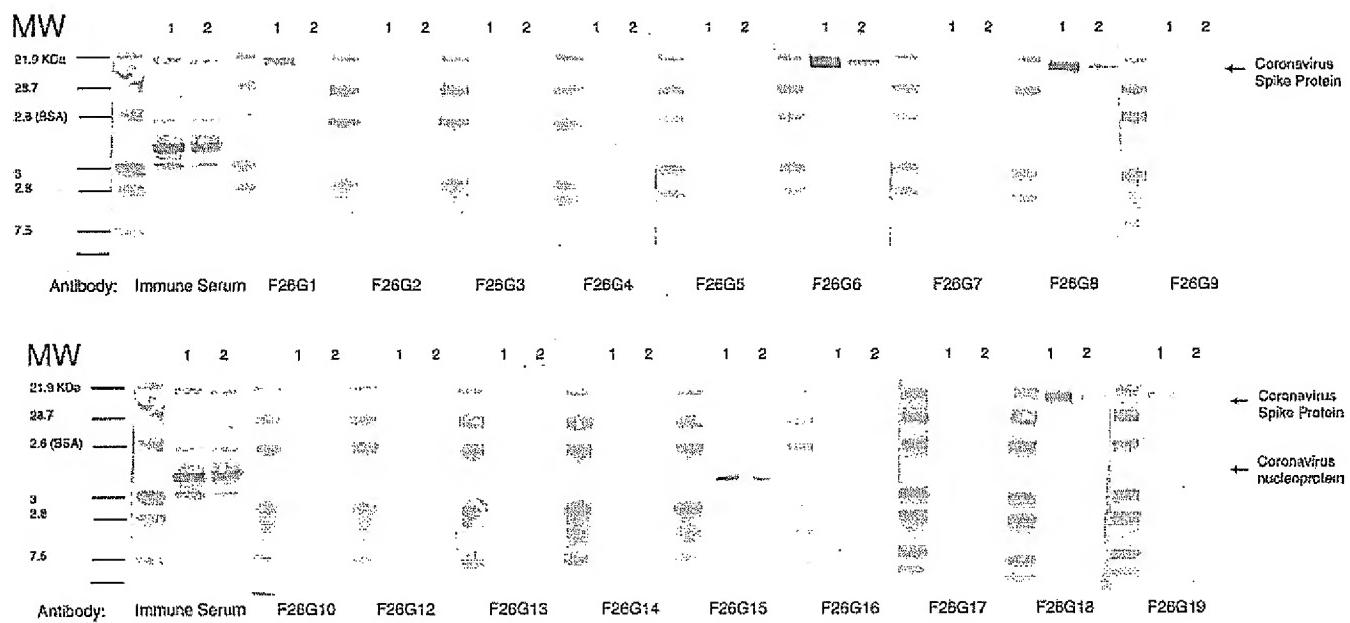
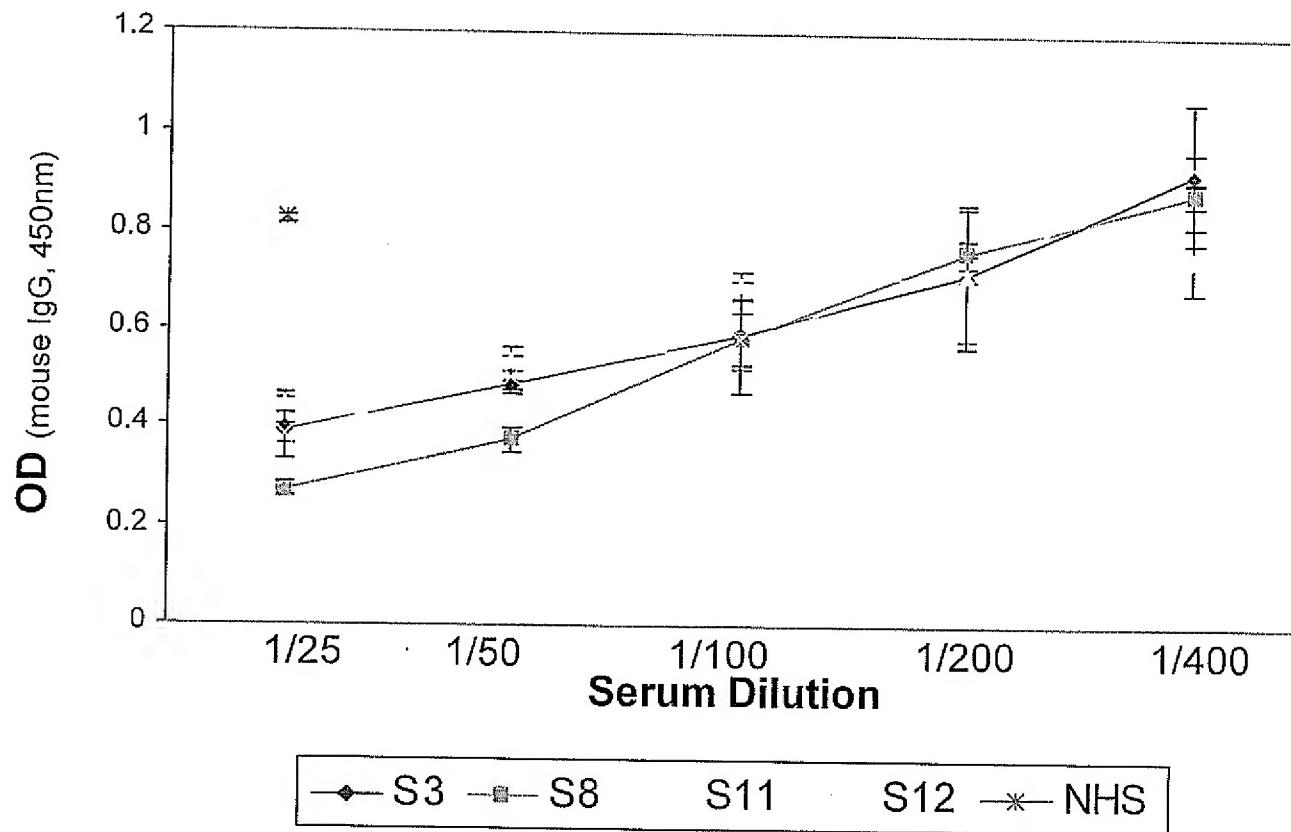


Figure 4

SARS NP C-ELISA



SARS Spike C-ELISA

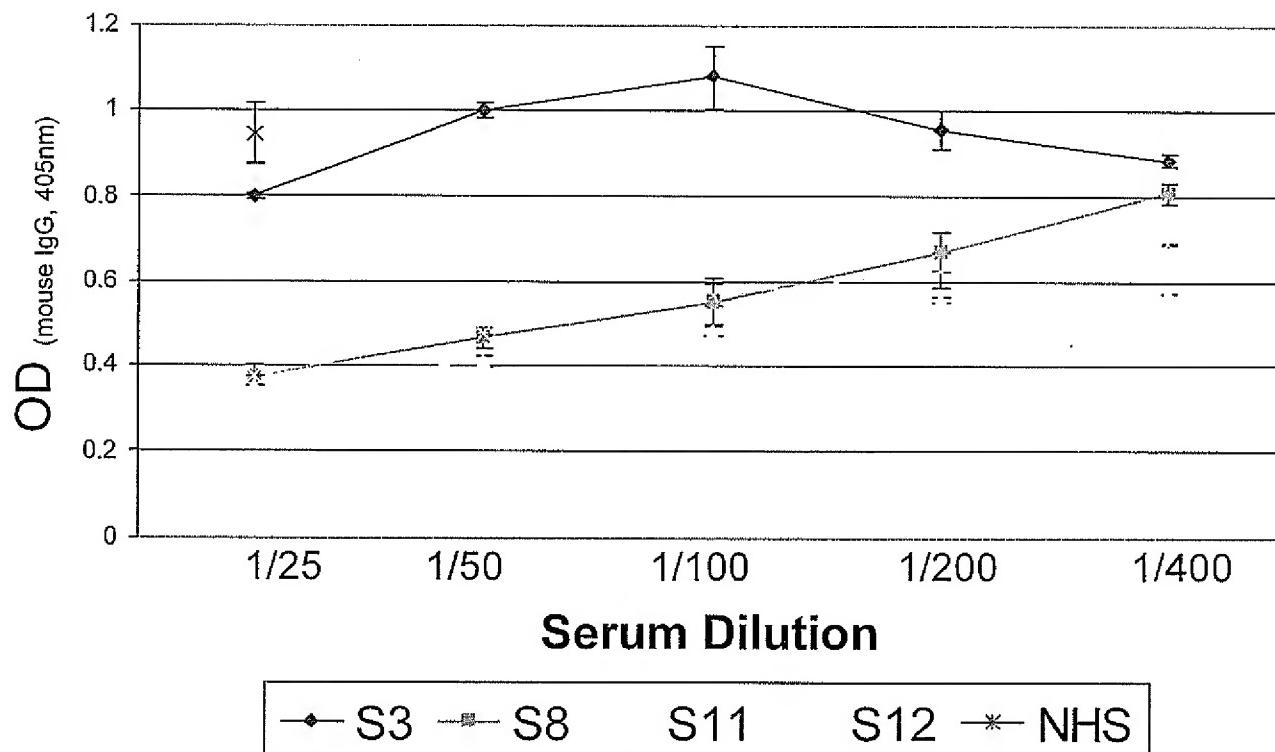


Figure 5

SARS CoV mAb V_L alignment

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FR 1          CDR1          FR 2          CDR2          FR 3          CDR3
*   20   *   40   *   60   *   80   *   100   *   120
G1_light : ELVMTQSPVSVITASGERKVTITCRASSISNN---YLHUYQQKPSSSPRLIYRTSILASGVLDFTSGSGSESTUTISCMQDEVALLYCQQGSSSPPPVRNGDQAGNKIG-----: 110
G3_light : DILMTQSPTSFAVSLGQRATISCRTSQSVSTSYNSYHUYQQKPQGPDPKLLIKYASNLTESGVPARPSGSGSDFTINIHVEGDTATYCCQHSWEIPLCJFGGTKEIKRADAAPTVS-----: 120
G6_light : ELVMTQSPASLISVATGKRVTIRCISSTDIDD----DHWYQQKAGKPPKLISEGNTISFGVPSRFSQSSQGNTIVFTVENTLSEMDAQNCLQSDNHPFTGGTKEIKRADAAPTVS-----: 116
G7_light : ELVMTQSPSSLSASLGERVSLTCRASQEISG---YLSQLQKPDGTIRKLIYASTLDSGVPKRTRSGRSGSMSLTISSLESDFAVYCLQVISYPUTFGGTKEIKRADAAPTVS-----: 116
G8_light : ELVMTQSPASLISVITGKRVTIRCISNTIDDD----DLNUSOLKAGEPPKKLISEGNTISFGVPSRFSQSSQGNTIVFTVENTLSEMDAQNCLQSDNHPFTGGTKEIKRADAAPTVS-----: 116
G10_light : DILMTQSHKFWMSTVGDRVISITCKASQDVST----AVAUYQOKPGCSPKKLILYWAISTRHTGVDPRFTGSGSDTWTITLTISSVOAEDALYYCOHYSTPYTFGGTKEIKRADAAPTVS-----: 116
G15_light : ELVMTQSPASLISASVGETWITICRASGNIRH----YLAUYYQOKQGSPQOLVNAKTLADGVPSRFSGSGSGTOSLKRINSLOSEDIGSYCQHFVISPYTFGGTKEIKRADAAPTVS-----: 116
G18_light : ELVMTQSPSSLSASLGDRVITSCRASQDISN---YLNUYQQKPDGTVKLILYYTSRLHAGVPSRSGSGSGTDYSLTISNLQEDITYFCQQGYTLPTYTFGGTKEIKRADAAPTVS-----: 125
    
```

Figure 6A

SARS CoV mAb V_H alignment

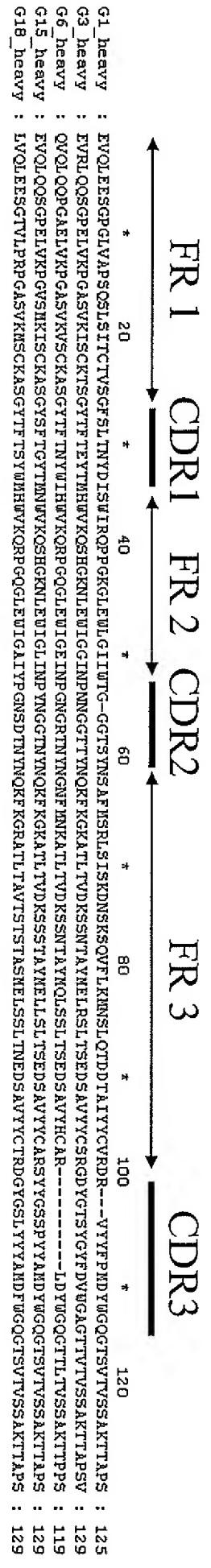
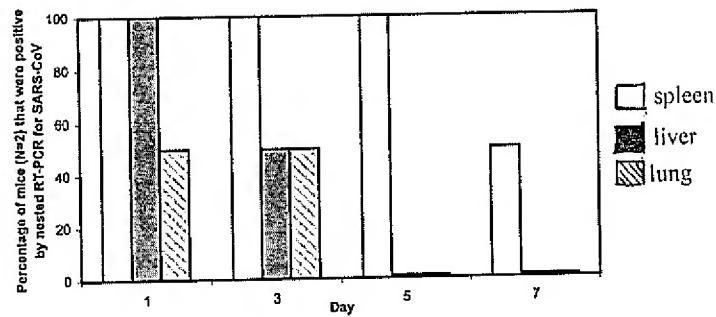
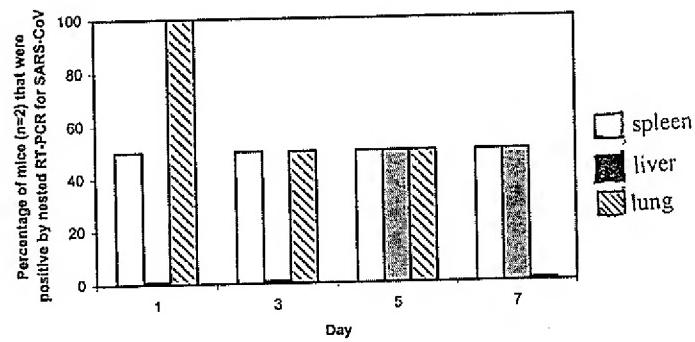


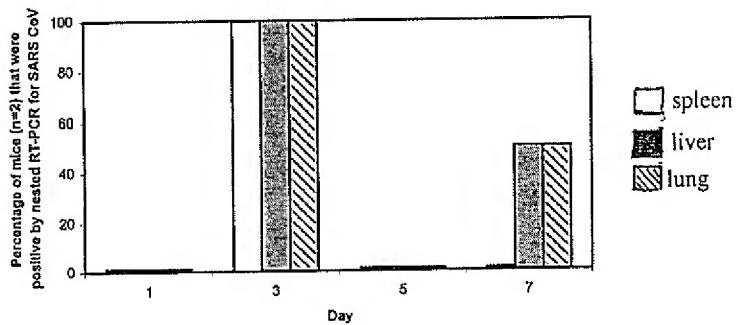
Figure 6B



(A)



(B)



(C)

FIGURE 11

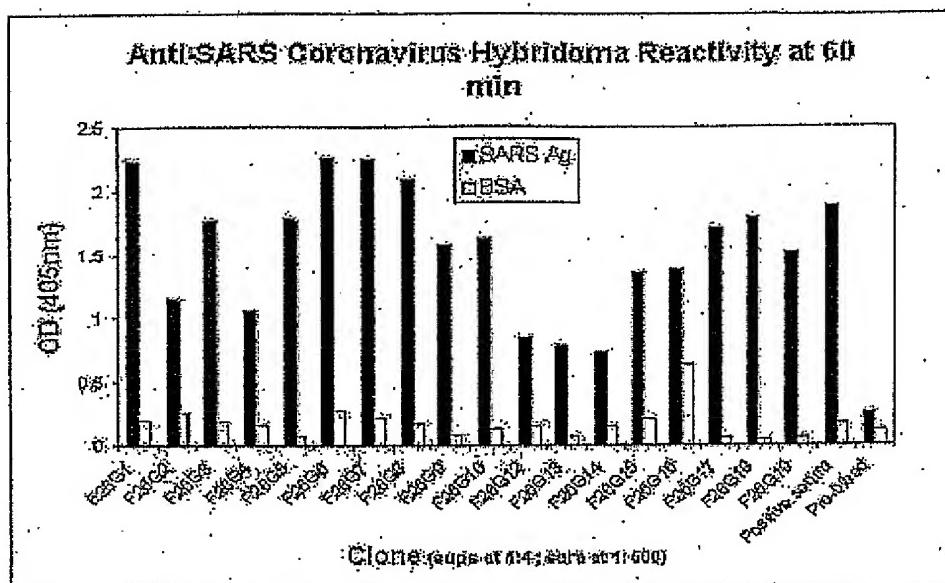


FIGURE 1

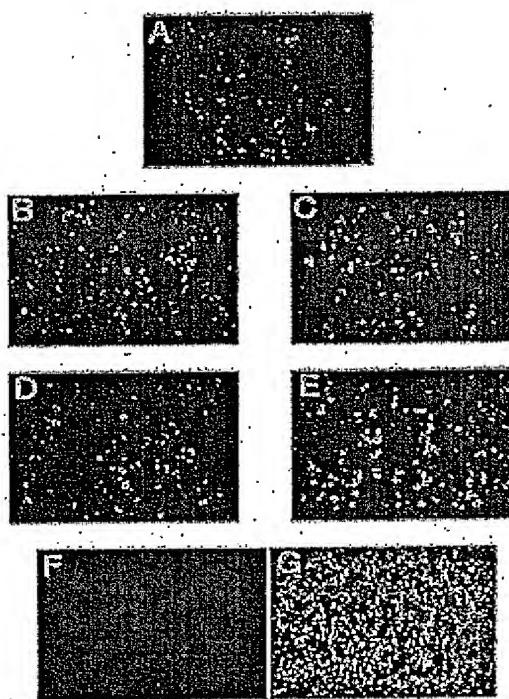


FIGURE 2

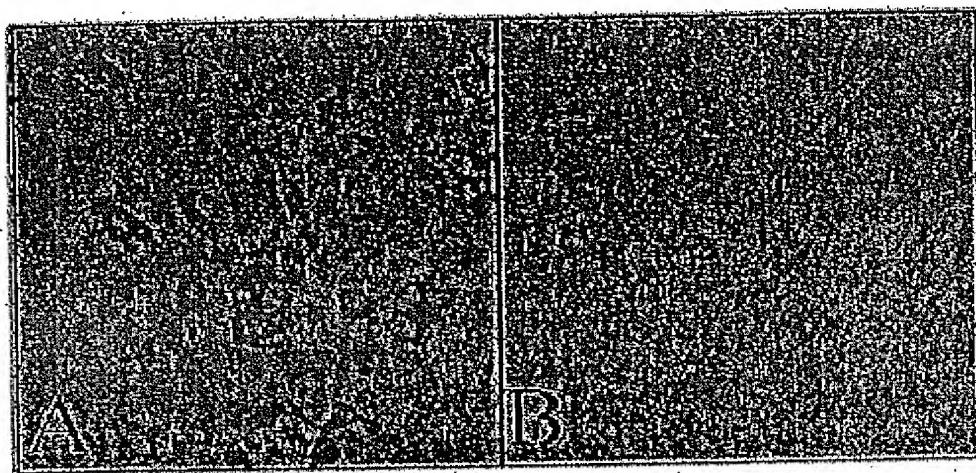


FIGURE 3

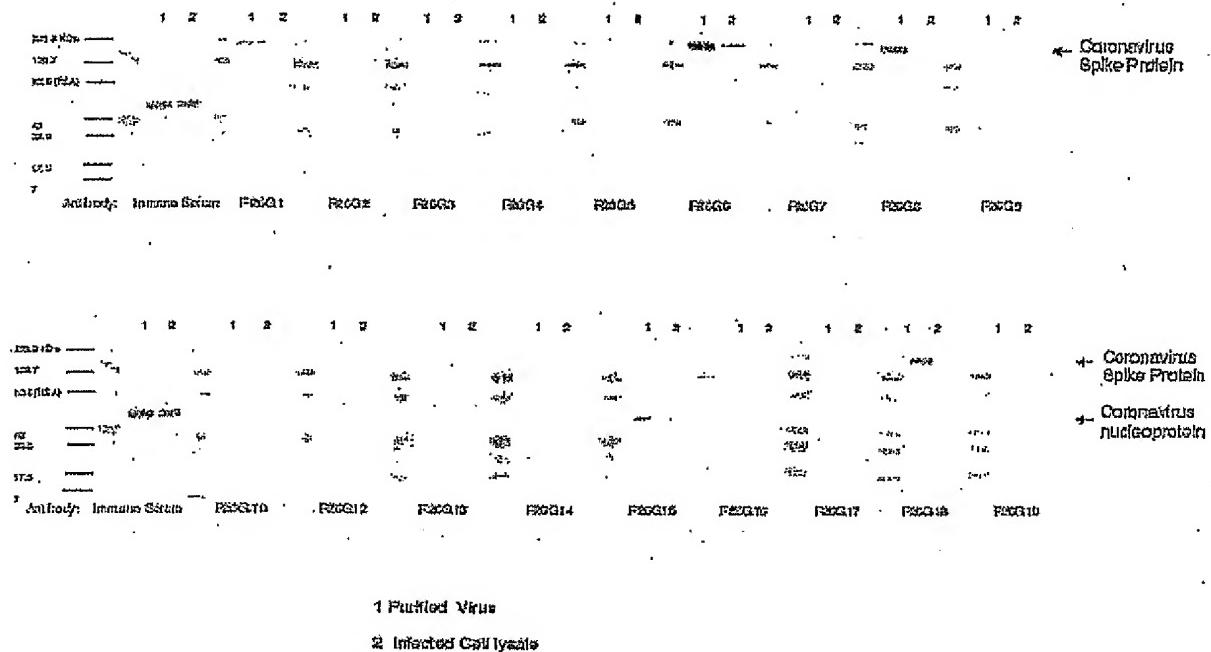


FIGURE 4

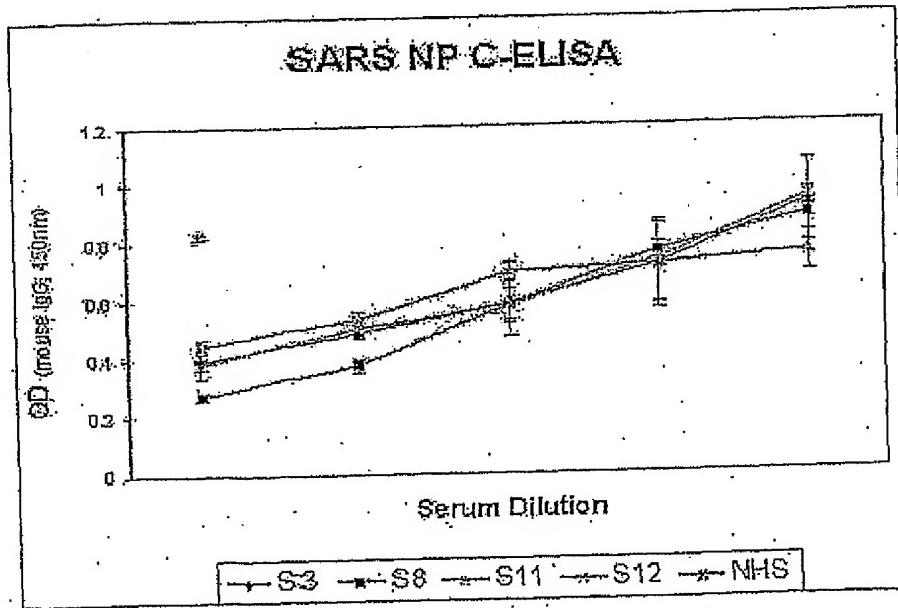
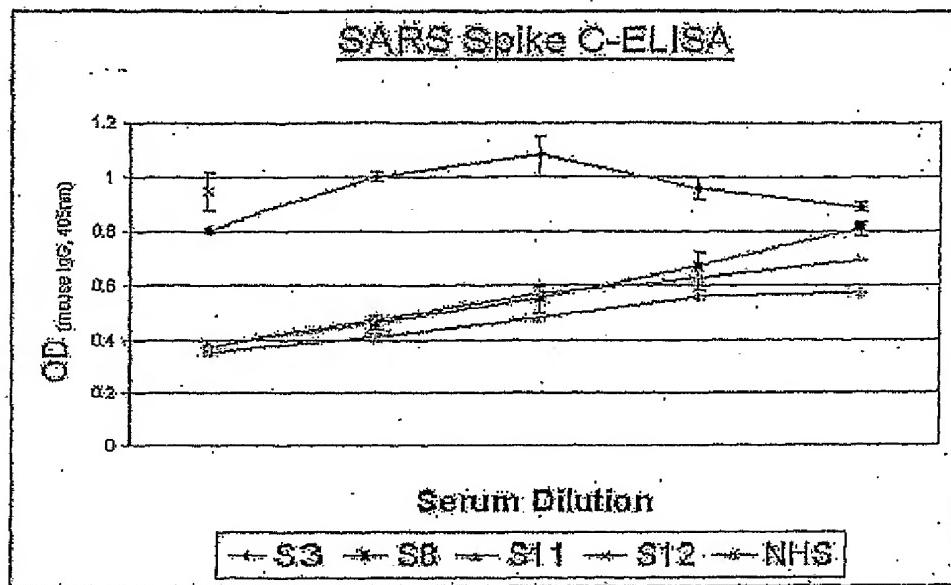
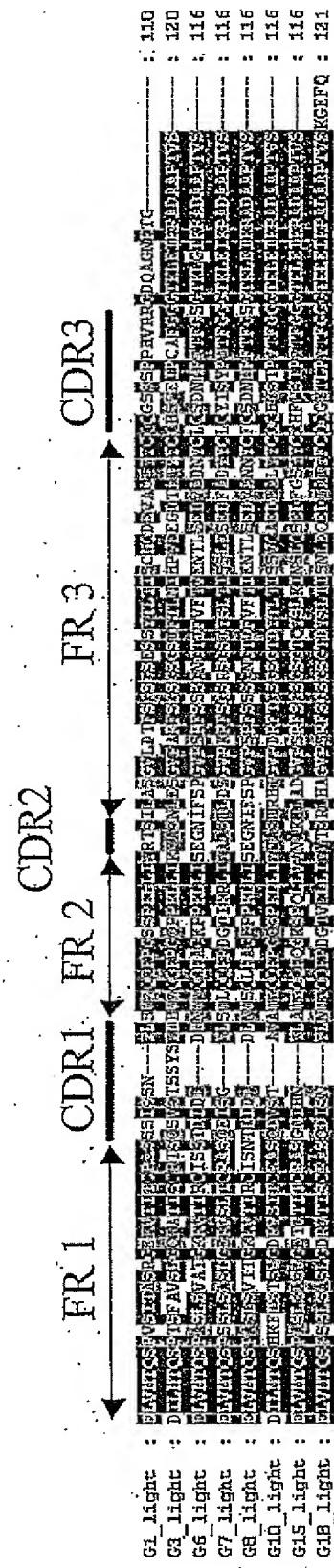


FIGURE 5

SARS CoV mAb V_L alignment



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WO 2005/054469

PCT/CA2004/002084

FIGURE 6A

SARS-CoV mAb V_H alignment

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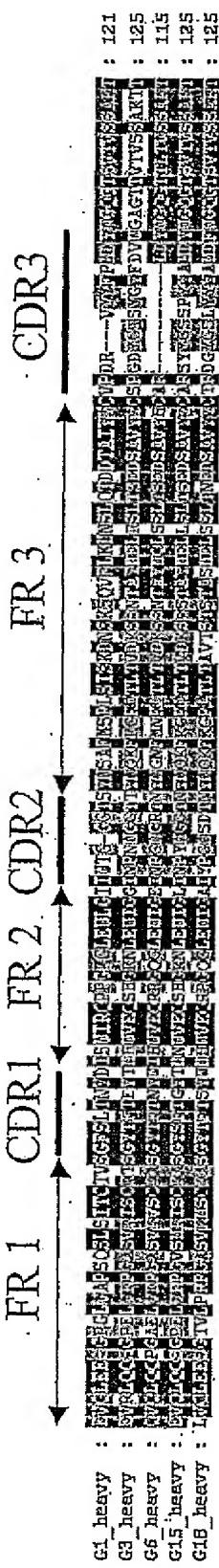
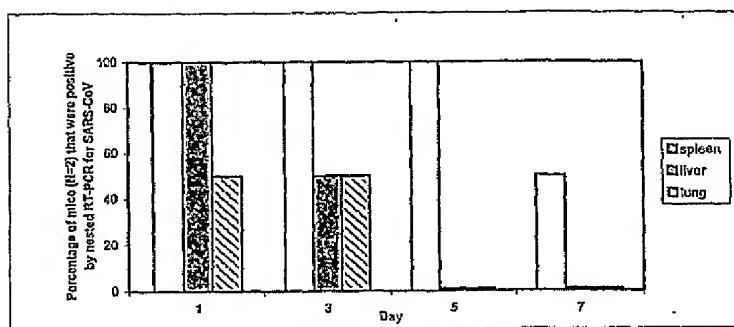
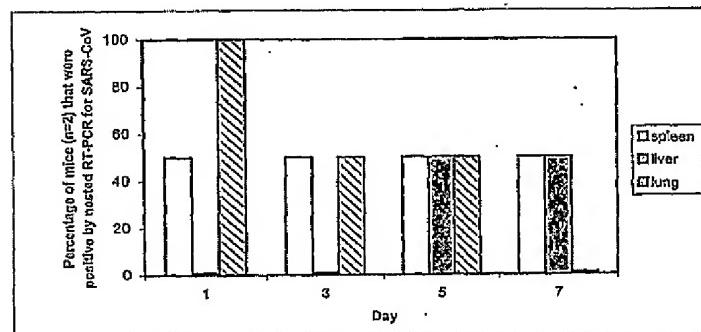


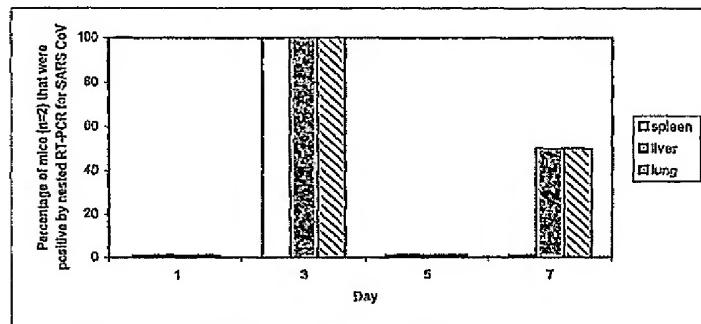
FIGURE 6 B



(A)



(B)



(C)

FIGURE 11